v) joining computationally overlapping common peptide sequences to obtain extended conserved peptide sequences,

vi) annotating secondary structure of extended conserved peptide sequences based on a crystal structure database,

vii) comparing pathogenic strain proteomes against proteomes of non-pathogenic strains and selecting at least one conserved peptide sequence not commonly conserved in these two groups,

viii) validating computationally at least one conserved peptide sequence as a potential drug target sequence by searching for a given conserved sequences in the host proteome and rejecting sequences present in the host proteome.

2. The method of claim 1 wherein 'N' is at least 4.

B1 Cont'd

3. The method of claim 1 wherein the selected organisms include at least one of: Mycoplasma pneumoniae, Helicobacter pylori, Hemophillus influenzae, Mycobacterium tuberculosis, Mycoplasma genitalium, Bacillus subtillis, Escherichia coli.

B2

4. A method as claimed in claim 1 where conserved peptide sequences include one or more of:

SUB D1

1.	**AAQSIGEPGTQLT**	35.	**KMSKSKGN**
2.	**AGDGTTTAT**	36.	**KMSKSLGN**
3.	**AGRHGNKG**	37.	**KNMITGAAQMDGAILVV**
4.	**AHIDAGKTTT**	38.	**KPNSALRK**
5.	**CPIETPEG**	39.	**LFGGAGVGKTV**
6.	**DEPSIGLH**	40.	**LGPSGCGK**
7.	**DEPTSALD**	41.	**LHAGGKFD**
8.	**DEPTTALDVT**	42.	**LIDEARTPLIISG**
9.	**DHAGIATQ**	43.	**LLNRAPTLH**
10.	**DHPHGGGEG**	44.	**LPDKAIDLIDE**
11.	**DLGGGTFD**	45.	**LPGKLADC**
12.	**DVLDTWFSS**	46.	**LSGGQQQR**
13.	**ERERGITI**	47.	**MGHVDHGKT**
14.	**ERGITITSAAT**	48.	**NADFDGDQMAVH**
15.	**ESRRIDNQLRGR**	49.	**NGAGKSTL**

16.	FSGGQRQR	50.	NLLGKRVD
17.	GEPGVGKTA	51.	NTDAEGRL
18.	GFDYLRDN	52.	PSAVGYQPTLA
19.	GHNLQEHS	53.	QRVALARA
20.	GIDLGTTNS	54.	QRYKGLGEM
21.	GINLLREGLD	55.	RDGLKPVHRR
22.	GIVGLPNVGKS	56.	SALDVSIQA
23.	GKSSLLNA	57.	SGGLHGVG
24.	GLTGRKIIVDTYG	58.	SGSGKSSL
25.	GPPGTGKTLLA	59.	SGSGKSTL
26.	GPPGVGKT	60.	SVFAGVGERTREGND
27.	GSGKTTLL	61.	TGRTHQIRVH
28.	GTRIFGPV	62.	TGVSGSGKS
29.	IDTPGHVDFT	63.	TLSGGEAQRI
30.	ILAHIDHGKSTL	64.	TNKYAEGYP
31.	INGFGRIGR	65.	TPRSNPATY
32.	IREGGRTVG	66.	VEGDSAGG
33.	IVGESGSGKS	67.	VRKRPGMYIG
34.	KFSTYATWWI		

B3 Cont'd

5. A method as claimed in claim 1 comprising increasing the number of [invariant] conserved peptide sequences by increasing the relatedness among the organisms being compared.

B3

6. A method as claimed in any one of claims 1-4 wherein the invariant sequences belong to at least one of the following proteins:

I DNA DIRECTED RNA POLYMERASE BETA CHAIN

II EXCINUCLEASE ABC SUBUNIT A

III EXCINUCLEASE ABC SUBUNIT B

IV DNA GYRASE SUBUNIT B

V ATP SYNTHASE BETA CHAIN

VI S-ADENOSYLMETHIONINE SYNTHETASE

VII GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE

VIII ELONGATION FACTOR G (EF-G)

IX ELONGATION FACTOR TU (EF-TU)

X 30S RIBOSOMAL PROTEIN S12

XI 50S RIBOSOMAL PROTEIN L12

XII 50S RIBOSOMAL PROTEIN L14

XIII VALYL tRNA SYNTHETASE (VALRS)

XIV CELL DIVISION PROTEIN FtSH HOMOLOG

XV DnaK PROTEIN (HSP70)

B3

XVI GTP BINDING PROTEIN LepA

XVII TRANSPORTER

XVIII OLIGOPEPTIDE TRANSPORT ATP BINDING PROTEIN OPPF

7. A method as claimed in claim 1 wherein the said method of comparing the peptide libraries as given in step (iii) of claim 1 is carried out by following the steps:

- selecting organism names from a menu;
- iteratively comparing peptide sequences of a first organism to peptide sequences of a second organism and for matching sequences, writing sequences to a file for the first organism and to a file for the second organism.

8. A method as claimed in claim 1 wherein the said method of locating the common peptides in the original protein sequences as given in step (iv) of claim 1 is carried out by following the steps:

- selecting protein sequences;
- iteratively comparing matched peptide sequences to protein sequences;
- where the peptide exists in a protein sequence writing the peptide PID, location and organism in a file associated with that peptide.

B3

9. A method as claimed in claim 1 wherein the said method of creating a common peptide of variable length after removing the overlapping as given in step (v) of claim 1 is carried out by following the steps:

- iteratively comparing data on matched peptide locations;
- determining overlapping matched peptides; and
- determining extended peptide sequences based on overlapping matched peptide sequences.